```
ccccgccgtg agtgagctct caccccagtc agccaaatga gcctcttcgg gcttctcctg 60

gtgacatctg ccctggccgg ccagagacga gggactcagg cggaatccaa cctgagtagt 120

aaattccagt tttccagcaa caaggaacag aacggagtac aagatcctca gcatgagaga 180

attattactg tgtctactaa tggaagtatt cacagcccaa ggtttcctca tacttatcca 240

agaaatacgg tcttggtatg gagattagta gcagtagagg aaaatgtatg gatacaactt 300

acgtttgatg aaagatttgg gcttgaagac ccagaagatg acatatgcaa gtatgatttt 360

gtagaagttg aggaacccag tgatggaact atattagggc gctggtgtgg ttctggtact 420

gtaccaggaa aacagatttc taaaggaaat caaattagga taagatttgt atctgatgaa 480

tattttcctt ctgaaccagg gttctgcatc cactacaaca ttgtcatgcc acaattcaca 540

gaagctgtga gtccttcagt gctacccccct tcagctttgc cactggacct gcttaataat 600

gctataactg cctttagtac cttggaagac cttattcgat atcttgaacc agagagatgg 660

cagttggact tagaagatct atataggcca acttggcaac ttcttggcaa ggcttttgtt 720

tttggaagaa aatccagagt ggtggatctg aaccttctaa cagaggaggt aagattatac 780

agctgcacac ctcgtaactt ctcagtgtcc ataagggaag aactaaagag aaccgatacc 840

attttctggc caggttgtct cctggttaaa cgctgtggtg ggaactgtgc ctgttgtctc 900

cacaattgca atgaatgtca atgtgtccca agcaaagtta ctaaaaaata ccacgaggtc 960

cttcagttga gaccaaagac cggtgtcagg ggattgcaca aatcactcac cgacgtggcc 1020

ctggagcacc atgaggagtg tgactgtgtg tgcagaggga gcacaggagg atagccgcat 1080

caccaccagc agctcttgcc cafafctgtg cagtgcagtg gctgattcta ttagagaacg 1140

tatgcgttat ctccatcctt aatctcagtt gtttgcttca aggacctttc atcttcagga 1200
```

FIG. 1A

```
tttacagtgt attctgaaag aggagacatc aaacagaatt aggacttgtg caacagctct 1260

tttgagagga ggcctaaagg acaggagaaa aggtcttcaa tcgtggaaag aaaattaaat 1320

gttgtattaa atagatcacc agctagtttc agagtcacca tgtacgtatt ccactagctg 1380

ggttctgtat ttcagttctt tcgatacggc ttagggtaat gtcagtacag gaaaaaaact 1440

gtgcaagtga gcacctgatt ccgttgcctt gcttaactct aaagctccat gtcctgggcc 1500

taaaatcgta taaaatctgg attttttttt tttttttttgc tcatattcac atatgtaaac 1560

cagaacattc tatgtactac aaacctggtt tttaaaaagg aactatgttg ctatgaatta 1620

aacttgtgtc rtgctgatag gacagactgg atttttcata tttcttatta aaatttctgc 1680

catttagaag aagagaacta cattcatggt ttggaagaga taaacctgaa aagaagagtg 1740

gccttatcct cactttatcg ataagtgact ttatttgttt cattgtgtac attttatat 1800

tctccttttg acattataac tgttggcttt tctaatcttg ttaaatatat ctattttac 1860

caaaggtatt taatattctt ttttatgaca acttagatca actattttta gcttggtaaa 1920

tttttctaaa cacaattgtt atagccagag gaacaaagat ggatataaaa atattgttgc 1980

cctggacaaa aatacatgta tntccatccc ggaatggtgc tagagttgga ttaaacctgc 2040

attttaaaaa acctgaattg ggaaanggaan ttggtaaggt tggccaaanc ttttttgaaa 2100

ataattaa                                                       2108
```

FIG. 1B

```
Met Ser Keu Phe Gly Leu Leu Leu Cal Thr Ser Ala Leu Ala Gly Gln
 1               5                   10                  15

Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
         20                  25                  30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
         35                  40                  45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
     50                  55                  60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65              70                  75                  80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
             85                  90                  95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Gly Asp Phe Val Glu Val Glu
         100                 105                 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
         115                 120                 125

Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
     130                 135                 140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145             150                 155                 160

Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
             165                 170                 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
         180                 185                 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
         195                 200                 205

Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
     210                 215                 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225             230                 235                 240

Leu thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
             245                 250                 255

Val Ser Ile Arg Glu Glu Leu Lye Arg Thr Asp Thr Ile Phe Trp Pro
         260                 265                 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
         275                 280                 285
```

FIG. 2A

```
His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lsy Lys
    290                 295                 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Cal Arg Gly Leu
305                 310                 315                 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
                325                 330                 335
Cys Val Cys Arg Gly Ser Thr Gly Gly
            340                 345
```

FIG. 2B

```
cgggtaaatt ccagttttcc agcaacaagg aacagaacgg agtacaagat cctcagcatg 60
agagaattat tactgtgtct actaatggaa gtattcacag cccaaggttt cctcatactt 120
atccaagaaa tacggtcttg gtatggagat tagtagcagt agaggaaaat gtatggatac 180
aacttacgtt tgatgaaaga tttgggcttg aagacccaga agatgacata tgcaagtatg 240
attttgtaga agttgaggaa cccagtgatg gaactatatt agggcgctgg tgtggttctg 300
gtactgtacc aggaaaacga atttctaaag gaaatcaaat taggataaga tttgtatctg 360
atgaatattt tccttctgaa ccagggttct gcatccacta caacattgtc atgccacaat 420
tcacagaagc tgtgagtcct tcagtgctac ccccttcagc tttgccactg gacctgctta 480
ataatgctat aactgccttt agtaccttgg aagaccttat tcgatatctt gaaccagaga 540
gatggcagtt ggacttagaa gatctatata ggccaacttg gcaacttctt ggcaaggctt 600
ttgtttttgg aagaaaatcc agagtggtgg atctgaacct tctaacagag gaggtaagat 660
tatacagctg cacacctcgt aacttctcag tgtccataag ggaagaacta aagagaaccg 720
ataccatttt ctggccaggt tgtctcctgg ttaaacgctg tggtgggaac tgtgcctgtt 780
gtctccacaa ttgcaatgaa tgtcaatgtg tcccaagcaa agttactaaa aaataccacg 840
aggtccttca gttgagacca aasaccggtg tcaggggatt gcacaaatca ctcaccgacg 900
tggccctgga gcaccatgag gagtgtgact gtgtgtgtag agggagcaca ggaggatagc 960
cgcatcacca ccagcagctc ttgcccagag ctgtgcagtg cagtggctga ttctattaga 1020
gaacgtatgc gttatctcca tcctaatct cagttgtttg cttcaaggac ctttcatctt 1080
caggatttac agtgcattct gaaagaggag acatcaaaca gaattaggag ttgtgcaaca 1140
gctctttgta gaggaggcct aaaggacagg agaaaaggtc ttcaatcgtg gaaagaaaat 1200
taaatgttgt attaaataga tcaccagcta gtttcagagt taccatgtat gtattccact 1260
agctggggttc tgtatttcag ttctttcgat acggcttagg gtaatgtcag tacaggaaaa 1320
aaactgtgca agtgagcacc tgattccgtt gccttgctta actctaaagc tccatgtcct 1380
gggcctaaaa tcgtataaaa tctggatttt tttttttttt tttgctcata ttcacatatg 1440
taaaccagaa cattctatgt actacaaacc tggttttaa aaaggaacta tgttgctatg 1500
aattaaactt gtgtcatgct gataggacag actgga 1536
```

FIG.3

```
Gly Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp
1               5                   10                  15
Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His
                20                  25                  30
Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn The Val Leu Val Trp
        35                  40                  45
Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp
    50                  55                  60
Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp
65                  70                  75                  80
Phe Val Glu Val Glu Glu Pro Ser Asp Gly The Ile Leu Gly Arg Trp
                85                  90                  95
Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln
            100                 105                 110
Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly
        115                 120                 125
Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val
        130                 135                 140
Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn
145                 150                 155                 160
Asn Ale Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu
                165                 170                 175
Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr
            180                 185                 190
Trp Gln Leu Leu Glu Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val
        195                 200                 205
Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr
    210                 215                 220
Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp
225                 230                 235                 240
the Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn
                245                 250                 255
Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser
            260                 265                 270
Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr
        275                 280                 285
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His
    290                 295                 300
His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly
305                 310                 315
```

<p align="center">FIG.4</p>

```
cacctggaga cacagaagag ggctctagga aaaatttttgg atggggatta tgtggaaact 60
accctgcgat tctctgctgc cagagccggc caggcgcttc caccgcagcg cagcctttcc 120
ccgggctggg ctgagccttg gagtcgtcgc ttccccagtg cccgccgcga gtgagccctc 180
gccccagtca gccaaatgct cctcctcggc cctcctcggc ctcctcctgc gctggccggc 240
caaagaacgg ggactcgggc tgagtccaac ctgagcagca agttgcagct ctccagcgac 300
aaggaacaga acggagtgca agatccccgg catgagagag ttgtcactat atctggtaat 360
gggagcatcc acagcccgaa gtttcctcat acgtacccaa gaaatatggt gctggtgtgg 420
agattagttg cagtagatga tatagtgcgg atccagctga catttgatga gagatttggg 480
ctggaagatc cagaagacga tatatgcaag tatgattttg tagaagttga ggagcccagt 540
gatggaagtg ttttaggacg ctggtgtggt tctgggactg tgccaggaaa gcagacttct 600
aaaggaaatc atatcaggat aagatttgta tctgatgagt attttccatc tgaacccgga 660
ttctgcatcc actacagtat tatcatgcca caagtcacag aaaccacgag tccttcggtg 720
ttgccccctt catctttgtc attggacctg ctcaacaatg ctgtgactgc cttcagtacc 780
ttggaagagc tgattcggta cctagagcca gatcgatggc aggtggactt ggacagcctc 840
tacaagccaa catggcagct ttttgggcaag gctttcctgt atgggaaaaa aagcaaagtg 900
gtgaatctga atctcctcaa ggaagaggta aaactctaca gctgcacacc ccggaacttc 960
tcagtgtcca tacgggaaga gctaaagagg acagatacca tattctggcc aggttgtttt 1020
ctggtcaagt gctgtgtgagg aaattgtgcc tgttgtctcc ataattgcaa tgaatgtcag 1080
tgtgtcccac gtaaagttac aaaaaagtac catgaggtcc ttcagttgag accaaaaact 1140
ggagtcaagg gattgcataa gtcactcact gatgtggctc tggaacacca cgaggaatgt 1200
gactgtgtgt gtagaggaaa cgcaggaggg taactgcagc cttcgtagca gcacacgtga 1260
gcactggcat tctgtgtacc cccacaagca accttcatcc ccaccagcgt tggccgcagg 1320
gctctcagct gctgatgctg gctatggtaa agatcttact cgtctccaac caaattctca 1380
gttgtttgct tcaatagcct tcccctgcag gacttcaagt gtcttctaaa agaccagagg 1440
caccaanagg agtcaatcac aaagcactgc accg 1474
```

FIG.5

```
Met Leu Leu Leu Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
 1               5                   10                      15

Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
             20                  25                  30

Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
         35                  40                  45

Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
     50                  55                  60

His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65                  70                  75                      80

Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                 85                  90                      95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
             100                 105                 110

Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
         115                 120                 125

Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
     130                 135                 140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                     160

Ser Ile Ile Met Pro Gln ValThr Glu Thr Thr Ser Pro Ser Val Leu
             165                 170                 175

Pro Pro Ser Ser Leu Ser Lei Asp Leu Leu Asn Asn Ala Val Thr Ala
             180                 185                 190

Phe Ser Thr Leu Glu Glu Leu Ile Glu Arg Tyr Leu Glu Pro Asp Arg Trp
         195                 200                 205

Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
     210                 215                 220

Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225                 230                 235                     240

Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
             245                 250                 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
         260                 265                 270

Gly Cys Leu Leu Val Lys Arg Gln Gly Gly Asn Cys Ala Cys Cys Leu
     275                 280                 285
```

FIG. 6A

```
His Asn Cus Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
    290                     295             300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
305                 310                 315                 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
                325                 330                 335
Cys Val Cys Arg Gly Asn Ala Gly Gly
    .       340                 345
```

FIG. 6B

```
hPDGF-C   M S L F G L L L V T S A L A G Q R R G T Q A E S N L S S K F Q F S S N K E Q N G   40
mPDGF-C   M L L L G L L L I T S A L A G Q R T G T R R E S N L S S K L Q L S S Q K E O N G   40

hPDGF-C   V Q Q P O H E R L L T V S T N G S I H S P P F P H T Y F R N T V L V N R L V A V   80
mPDGF-C   V Q D P R M E R V V T I S G N G S T H S R K F P H T Y F R N M V L V N R L V A V   80

hPDGF-C   F E N V N I Q L T F D E R F G L E D P E D D I C K Y D F V E V E E P S D G T T S   120
mPDGF-C   G E N V R T Q L T F D E R F G L E D P E D D I C E Y D F V E V E E P S D G S V S   120

hPDGF-C   G R W C G S G T V F G K Q I S K G N O I R I R F V S D E Y F P S E P G F C I H Y   160
mPDGF-C   G R W C G S G T V F G K Q T S K G N H I R I R F V S D E Y E P S E P G F C I H Y   160

hPDGF-C   N I V M P Q F T E A V S P S V L P P S S L P L D L L N N A I T A F S T L F D L I   200
mPDGF-C   S I I M P Q V I E T T S P S V L P P S I L S L D L L N N A V T A F S T L F D L I   200

hPDGF-C   R Y L E P F R W Q L P L E O L Y E F T W Q L L C K A F V F G R K S R V V D L N L   240
mPDGF-C   R Y L E P D P W Q V P L P S L Y K P T W Q L L G F A F L Y G K K S N V V N L N L   240

hPDGF-C   L T E E V R L Y S C T P R N F S V S I R E E L K R T D T I F W P G G L L V K R C   280
mPDGF-C   L K F F V K L Y S C T P R N F S V S I R E E L K R T D T I F W P G G L L V K R C   280

hPDGF-C   G G N C A C C L R N C N E C O C Q C V P S K V T K K Y H E V L Q L R P K T G V R G Y   320
mPDGF-C   G G N C A C C L R V C N E C Q C V P R K V T K K Y H E V L O L R P K T G V R G Y   320

hPDGF-C   H E S L T D V A L E H H E E C D C V C R G S T G G   345
mPDGH-C   H E S L T D V A L E H H E E C D C V C R G N A G G   345
```

FIG.7

signal sequence

CUB domain | PDGF/VEGF Homology Domain

FIG.8

PDGF-A
PDGF-B
hPDGF-C PVDV
mPDGF-C PVDV
VEGF-C
VEGF-D
VEGF 165
PlGF-2
VEGF-B167
Pox Orf VEGF

54.7

| | | | | | |
0   10   20   30   40   50

Amino acid replacements (per 100 residues)
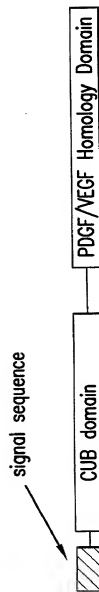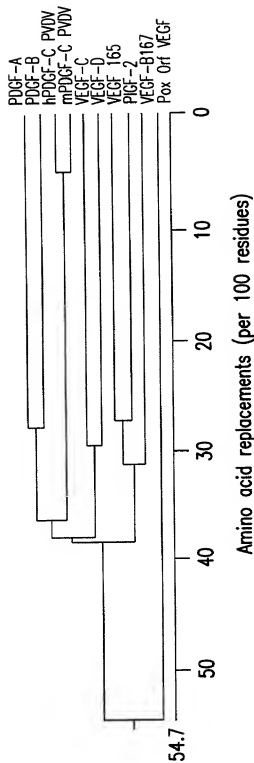
FIG.10

```
VEGF 165     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
PlGF-2       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
VEGF-B167    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
Pgx Crf VEGF - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
VEGF-C       M H L L G F F S V A C S L L A A A L L P G P R E A P A A A A                                    30
VEGF-D       - - - - - - - - - - - - - - - - - M Y G E W G M G N I L M M F H                                15
PDGF-A       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
PDGF-B       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
hPDGF-C PVDV - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
mPDGF-C PVDV - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1


VEGF 165     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
PlGF-2       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
VEGF-B167    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
Pox Orf VEGF - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
VEGF-C       A F E S G L D L S D A E P D A G E A T A Y A S K D L E E Q L                                    60
VEGF-D       V Y L V O G F R S E H G P Y K D F S F E R S S R S M L E R S                                    45
PDGF-A       - - - - M R T L A C L L L L G C G Y L A N V L A E E A E I P                                    26
PDGF-B       M N R C W A L F L S L C C Y L R L V S A E G D P I P E E L Y                                    30
hPDGF-C PVDV - - - - - - M P Q F T E A V S P S V L P P S A L P L D L L                                      23
mPDGF-C PVDV - - - - - - M P Q V T E T T S P S V L P P S A L S L D L L                                      23


VEGF 165     - - - - - - - - - - - - - - - - - - - - - M N F L L S W V E W                                  10
PlGF-2       - - - - - - - - - - - - - - - - - - - - - M P V M R L F P C F                                  10
VEGF-B167    - - - - - - - - - - - - - - - - - - - - - - - - M S P L L                                      5
Pox Orf VEGF - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                                    1
VEGF-C       R S V S S V D E L M T V L Y P E Y W K M Y K C Q L R K G G W                                    90
VEGF-D       E O O I R A A S S L E E L L O I A H S E D W K L W R C R L K                                    75
PDGF-A       R E V I E R L A R S Q I H S I R D L Q R L L E I D S V G S E                                    56
PDGF-B       E M L S D H S I R S F D D L O R L L H G D P - - - - - G E E                                    55
hPDGF-C PVDV N N A I T A F S T L E D L I R Y L E P E R W Q L D L E D L Y                                    53
mPDGF-C PVDV N N A V T A F S T L E E L I R Y L E P D R W Q V D L D S L Y                                    53


VEGF 165     S L A L L L Y L H H A K W S Q A A P M A E G G G Q N H H E V                                    40
PlGF-2       L Q L L A G L A L P A V P P Q Q W A L S A G N G S S E V E V                                    40
VEGF-B167    R R L L L A A L L Q L A P A Q A P V S Q P D A P G H Q R K V                                    35
Pox Orf VEGF - - - - - - M K L L V G I L V A V C L H Q Y L L N A D S N T                                  24
VEGF-C       Q H N R E Q A N L N S R T E E T I K F A A A H Y N T E I - L                                    119
VEGF-D       L K S L A S M D S R S A S H R S T R F A A T F Y D T E T - L                                    104
PDGF-A       D S L D T S L R A H G V H - - A T K H V P E K R P L R I R R                                    84
PDGF-B       D G A E L D L N M T R S H S G G E L E S L A R G R R S L G S                                    85
hPDGF-C PVDV R P T W Q L L G K A F V F G R K S R - - - - - - - V V D L                                    75
mPDGF-C PVDV K P T W Q L L G K A F L Y G K K S K - - - - - - - V V N L                                    75
```

FIG. 9A

```
VEGF 165        V K F M D V Y O R S Y C H P I E T L V D I F Q E Y P D E I E   70
PIGF-2          V P F Q E V W G R S Y C R A L E R L V D V V S E Y P S E V E   70
VEGF-B167       V S W I D V Y T R A T C Q P R E V V V P L T V E L M G T V A   65
Pox Orf VEGF    K G W S E V L K G S E C K P R P I V V P V S E T H P E L T S   54
VEGF-C          K S I D N E W R K T Q C M P R E V C I D V G K E F G V A T N   149
VEGF-D          K V I D E E W D R T Q C S P R E T C V E V A S E L G K T T N   134
PDGF-A          K R S I E E A V P A V C K T R T V I Y E I P R S Q V D P T S   114
PDGF-B          L T I A E P A M I A E C K T R T E V F E I S R R L I D R T N   115
HPDGF-C PVDV    N L L T E E V R L Y S C T P R N F S V S I - R E E L K R T D   104
mPDGF-C PVDV    N L L K E E V K L Y S C T P R N F S V S I - R E E L K R T D   104

VEGF 165        Y I F K - - P S C V P L M R C G G - - - C C N D E G L E C V   95
PIGF-2          H M F S - - P S C V S L L R C T G - - - C C G D E D L H C V   95
VEGF-B167       K Q L V - - P S C V T V Q R C G G - - - C C P D D G L E C V   90
Pox Orf VEGF    Q R F N - - P P C V T L M R C G G - - - C C N D E S L E C V   79
VEGF-C          T F F K - - P P C V S V Y R C G G - - - C C N S E G L Q C M   174
VEGF-D          T F F K - - P P C V N V F R C G G - - - C C N E E G V M C M   159
PDGF-A          A N F L I W P P C V E V K R C T G - - - C C N T S S V K C Q   141
PDGF-B          A N F L V W P P C V E V Q R C S G - - - C C N N R N V Q C R   142
hPDGF-C PVDV    T I F - - W P G C L L V K R C G G N C A C C L H N C N E C Q   132
mPDGF-C PVDV    T I F - - W P G C L L V K R C G G N C A C C L E N C N E C Q   132

VEGF 165        P T E E S N I T M Q I M R I K - - - P H Q G Q - - - - - H I   117
PIGF-2          P V E T A N V T M Q L L K I R - - - S G D R P - - - - - S Y   117
VEGF-B167       P T G Q H Q V R M Q I L M I R Y - - P S S Q L - - - - - - -   111
Pox Orf VEGF    P T E E V N V S M E L L G A S G S G S N G M Q - - - - - R L   104
VEGF-C          N T S T S Y L S K I L F E I T V - - P L S Q G - - - - - P K   197
VEGF-D          N T S T S Y I S K O L F E I S V - - P L T S V - - - - - P E   182
PDGF-A          P S R V H H R S V K V A K V E Y V R K K P K L - - - - - K E   166
PDGF-B          P T Q V Q L R P V Q V R K L E I V R K K P I F - - - - - K K   167
hPDGF-C PVDV    C V P - S K V T K K Y H E V L Q L R P K T G V R G L H K S L   161
mPDGF-C PVDV    C V P - R K V T K K Y H E V L Q L R P K T G V K G L H K S L   161

VEGF 165        G E M S F L Q H N K - C E C R P K K - - - - - - - - - D R   136
PIGF-2          V E L T F S Q H V R - C E C R P L R E - - - - K M K P E R R   142
VEGF-B167       G E M S L E E H S Q - C E C R P K K K - - - - - D S A V K P   135
Pox Orf VEGF    S F V E H K K - - - - C D C R P R F T - - - - - - - T T P P   123
VEGF-C          P V T I S F A N H T S C R C M S K L D - - - V Y R Q V H S I   224
VEGF-D          L V P V K I A N H T G C K C L P T G P - - - - - R H P Y S I   207
PDGF-A          V Q V R L E E H L E - C A C A T T S L N P D Y R E E D T G R   195
PDGF-B          A T V T L E D H L A - C K C E T V A A A R P V T R S P G G S   196
hPDGF-C PVDV    T D V A L E H H E E - C D C V C R G S T G G                   182
mPDGF-C PVDV    T D V A L E H H E E - C D C V C R G N A G G                   182
```

<div align="center">

FIG. 9B

</div>

```
VEGF  165     A R Q E N P C G P C S S E R R K H L F V Q D P Q T C K C S C   166
PlGF-2        R P K G R G K R R R E N Q R P T D C H L C G D A V P R R       170
VEGF-B167     D S P R P L C P R C T Q H H Q R P D P R T - - - - C R C R C   161
Pox Orf VEGF  T T T R P P R R R R                                          133
VEGF-C        I R R S L R A T - L P Q C Q A A N K I C P T N Y M W N N H I   253
VEGF-D        I R R S L Q T P E E D E C P H S K K L C P I D M L W D N T K   236
PDGF-A        P R E S G K K R K R K R L K P T                              211
PDGF-B        Q E Q R A K T P Q T R V T I R T V R V R R P P K G K H R K F   225
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF  165     K N T D S - R C K A R Q L E L N E R T C R C D K P R R         192
PlGF-2                                                                     170
VEGF-B167     R R R S F L R C Q G R G L E L N P D T C R C R K L R R         188
Pox Orf VEGF                                                               133
VEGF-C        C R C L A Q E D F M F S S D A G D D S T D G F H D I C G P N   283
VEGF-D        C K C V L Q D E - T P L P G T E D H S Y L Q E P T L C G P H   266
PDGF-A                                                                     211
PDGF-B        K H T H D K T A L K E T L G A                                241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF  165                                                                  192
PlGf-2                                                                     170
VEGF-B167                                                                  188
Pox Orf VEGF                                                               133
VEGF-C        K E L D E E T C Q C V C R A G L R P A S C G P H K E L D R N   313
VAGF-D        M T F D E D R - - - - - - - - - - - - - - - - - - - - - -    273
PDGF-A                                                                     211
PDGF-B                                                                     241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF  165                                                                  192
PlGF-2                                                                     170
VEGF-B167                                                                  188
Pox Orf VEGF                                                               133
VEGF-C        S C Q C V C K N K L F P S Q C G A N R E F D E N T C Q C V C   343
VEGF-D        - C E C V C K A P C P G D L I O H P E N - - - - - C S C F E   297
PDGF-A                                                                     211
PDGF-B                                                                     241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182
```

FIG. 9C

```
VEGF 165                                                                      192
PIGF-2                                                                        170
VEGF-B167                                                                     188
Pox Orf VEGF                                                                  133
VEGF-C        K R T C P R N Q P L N P G K C A C E C T E S P Q K C L L K G     373
VEGF-D        C K E S L E S C C Q K K K I - - - - - - - - - - - - - - -      312
PDGF-A                                                                        211
PDGF-B                                                                        241
hPDGF-C PVDV                                                                  182
mPDGF-C PVDV                                                                  182


VEGF 165                                                                      192
PIGF-2                                                                        170
VEGF-B167                                                                     188
Pox Orf VEGF                                                                  133
VEGF-C        K K F H H Q T C S C Y R R P C T N R Q K A C E P G F S Y S E     403
VEGF-D        - - F H P D T C S C E D R - C P F H T R T C A S R K P A C G     338
PDGF-A                                                                        211
PDGF-B                                                                        241
hPDGF-C PVDV                                                                  182
mPDGF-C PVDV                                                                  182


VEGF 165                                                                      192
PIGF-2                                                                        170
VEGF-B167                                                                     188
Pox Orf VEGF                                                                  133
VEGF-C        E V C R C V P S Y W K R P Q M S                                 419
VEGF-D        K H W R F P K E T R A Q G L Y S O E N P                         358
PDGF-A                                                                        211
PDGF-B                                                                        241
hPDGF-C PVDV                                                                  182
mPDGF-C PVDV                                                                  182
```

FIG. 9D

FIG. 11

Sequence alignment (mPDGF-C CUB, hPDGF-C CVB, hBMP-1 CUB1, hBMP-1 CUB2, hBMP-2 CUB3, Neuropilin CUB1, Neuropilin CUB2)

Block 1:

Label	Sequence	No.
mPDGF-C CUB	ERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRI	85
hPDGF-C CVB	ERITTIVSITNGSIHSPRFPHTYPRNTIVWRLVAVEENVWI	59
hBMP-1 CUB1	CGGDVKKDYIGNLINGSITISPGWPXEYPIPNKNCIWRLIOVSEGF – HV	473
hBMP-1 CUB2	CGGFLTKLNESPICYLTSPGYPMSIYHPSEKCEWLIQAPDPYQR	629
hBMP-2 CUB3	GDTIKIIESPICYLTSPGYPMSIYHPSEKCEWLIQAPDPYQR	167
Neuropilin CUB1	CSQNYTTPSGVIKSPGFPEEYPNSLCCTYIVPAPXMSE – IT	195

Block 2:

Label	Sequence	No.
mPDGF-c cub	QLTFDERDGLED – – – PEDDOCKYPVEVEE – – PSDGSVL	120
hPDGF-C CUB	QLTFDERFGLED – – – PEDDICKYDFVEVEE – – PSDGTIL	93
hBMP-1 CUB1	ILNFTS – LDLYRSA – – – LICWYDYLEVRDCPWAKAPLR	393
hBMP-1 CUB2	GLTFQS – FEIERND – – – SCAIYDYLEVRDGHSESSTLI	506
hBMP-1 CUB3	SLIQFDF – FEIEGND – – – VCKYDFVEVFDGENENGHFR	100
Neuropilin CUB1	MINFNPHFDLEDRD – – – CKYDFVKVYDGENENGHFR	224
Neuropilin CUB2	ILEFESF – DLEPDSNPPCCMFCRYDRLHIWDGFPDVGPHI	224

Block 3:

Label	Sequence	No.
mPDGF-C cub	GRWCGGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY	160
hPDGF-C CUB	GRWCGGSGTVPGEITSKGNQIRIRFVSDEYFPSEPGFCIHY	133
hBMP-1 CUB1	CRIFCGS – KLIPEIVISTDSRLWVEFRSSSNWVGK – GFAVIY	431
hBMP-1 CUB2	GRYCGGS – Y – EKPDDIKISTSSRLWLKFVSDGSINKA – GFAVNY	544
hBMP-1 CUB3	GKFCGGSI – EKPEVITSQYNNMRVEFXSDNTVSKK – GFKAHF	700
Neuropilin CUB1	GKFCGCGK – IAPPPVVSISGPFLFLIKFVSDYETKGA – GFSIRY	138
Neuropilin CUB2	GKYCGQ – KTPGRIRSSGILSMVFYTDAIAKEANY	262

Block 4:

Label	Sequence	No.
mPDGF-C CUM	SII	163
hPDGF-C CUB	MIV	136
hBMP-1 CUB1	EAIL	434
hBMP-1 CUB2	FK	546
hBMP-1 CUB3	FSE	703
Neuropilin CUB1	– ETT	140
Neuropilin CUB2	SVL	265

FIG. 12

- 7.5
- 4.4
- 2.4
- 1.35

HEART | BRAIN | PLACENTA | LUNG | LIVER | SKELETAL MUSCLE | KIDNEY | PANCREAS | SPLEEN | THYMUS | PROSTATE | TESTIS | OVARY | SM. INTESTINE | COLON | PBL
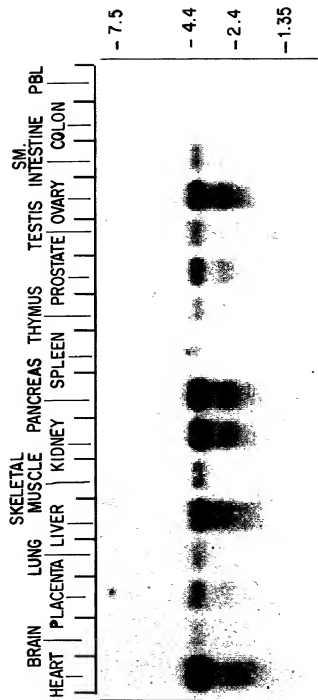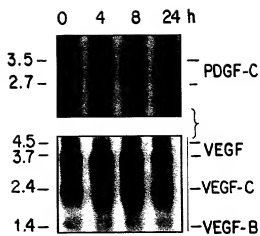
FIG. 13
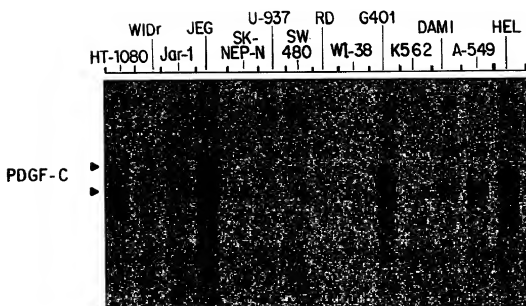
FIG. 14
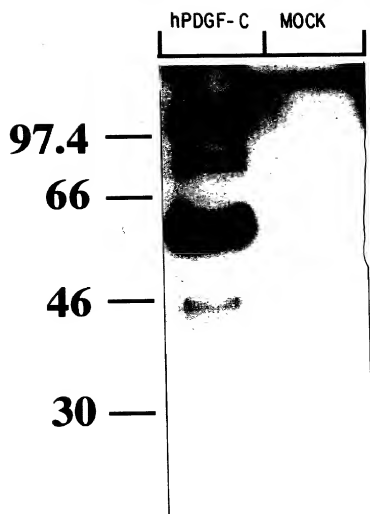
FIG. 15
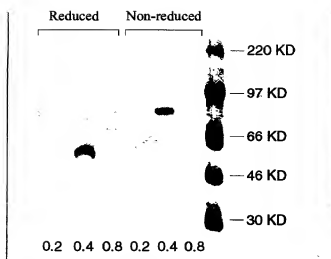
FIG. 16A
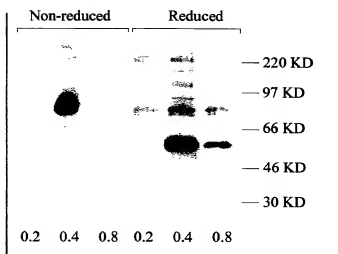
FIG. 16B
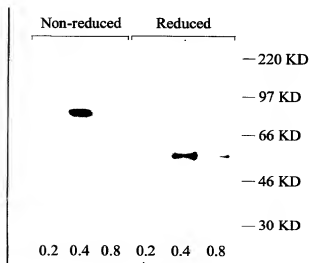
FIG. 16 C
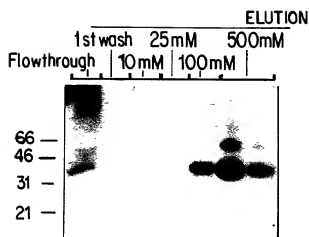
FIG. 17A
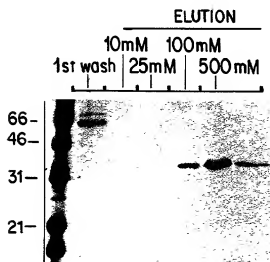
FIG. 17B

FIG. 17C

FIG. 18

FIG. 19

NO STIMULATION

PDGF-AA (10 ng/ml)

fl PDGF-CC (100 ng/ml)

cPDGF-CC (100 ng/ml)

PDGF-AA (10 ng/ml)+

cPDGF-CC (100 ng/ml)
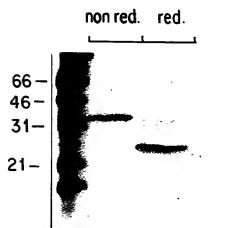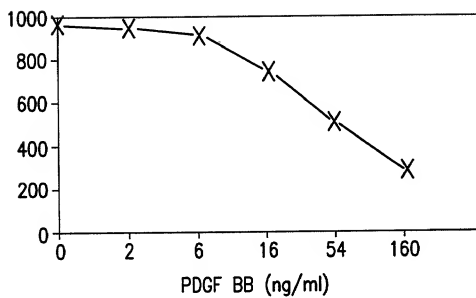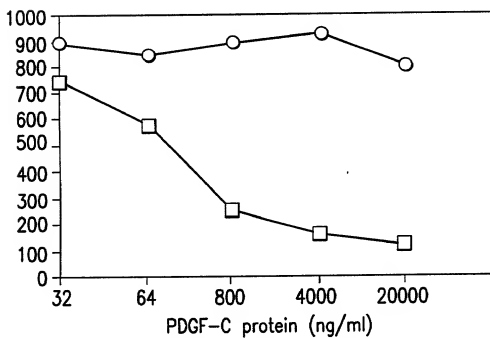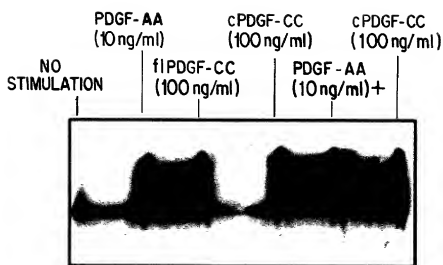
IP : PDGF alpha-rec.
IB: P-T yr

FIG. 20
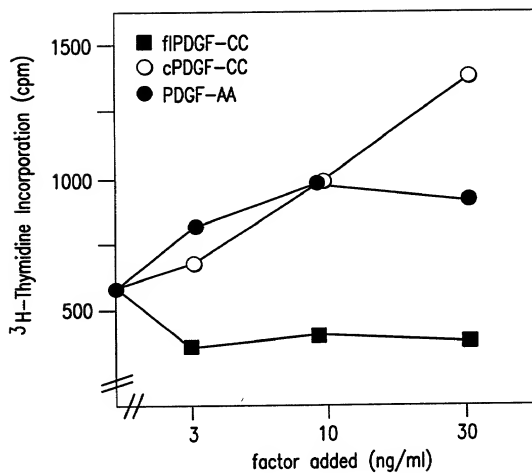
FIG. 21
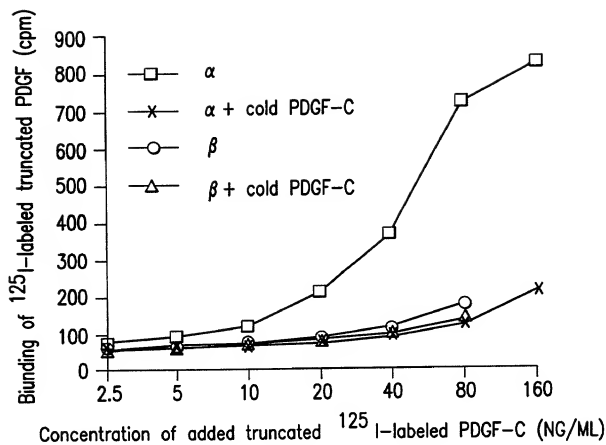
FIG. 22
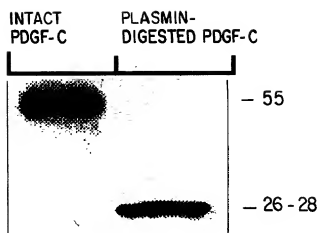
FIG. 23
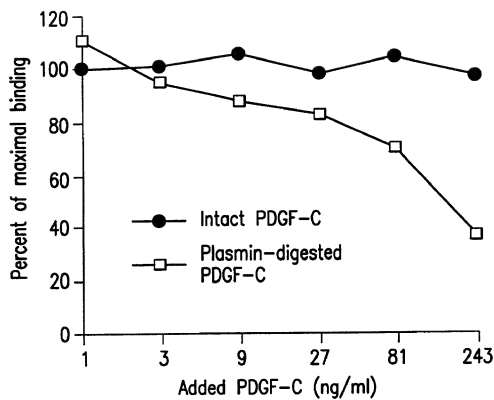
FIG. 24
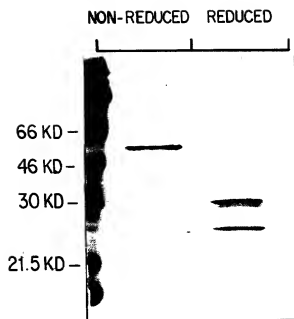
FIG. 25

FIG. 26A

FIG. 26B

FIG. 26C

FIG. 26D

FIG. 26E
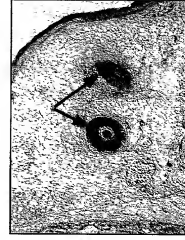
FIG. 26F
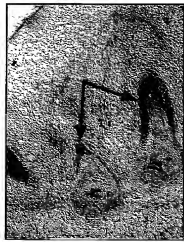
FIG. 26 G
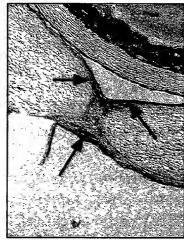
FIG. 26 H

FIG. 26 I
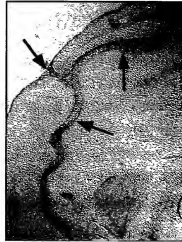
FIG. 26 J

FIG. 26 K
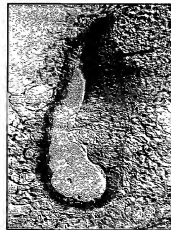
FIG. 26 L
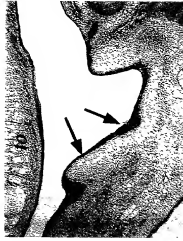
FIG.26 O

FIG. 26N
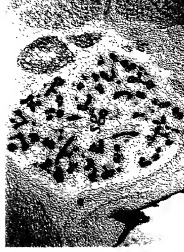
FIG. 26 M

FIG. 26Q
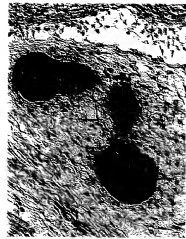
FIG. 26P

FIG. 26 R

FIG. 26S

FIG. 26T
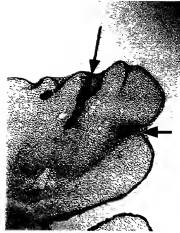
FIG. 26U

FIG. 26 V
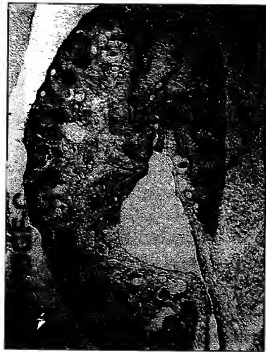
FIG. 27B

FIG. 27D

FIG. 27A

FIG. 27C

FIG.27E

FIG. 27F

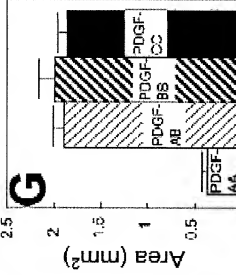FIG. 28A

PDGFR-α -/-
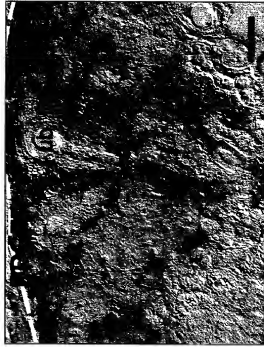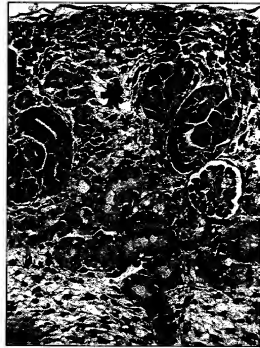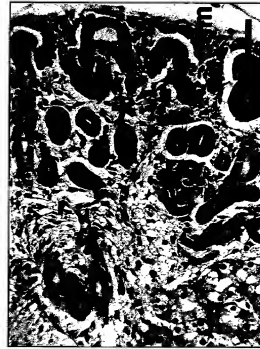
FIG. 28B

FIG. 28C

FIG. 28D

FIG. 28E
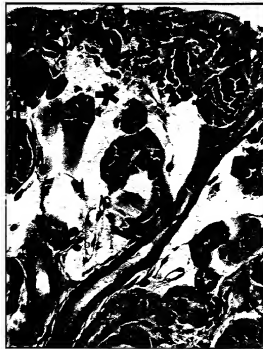
FIG. 28F
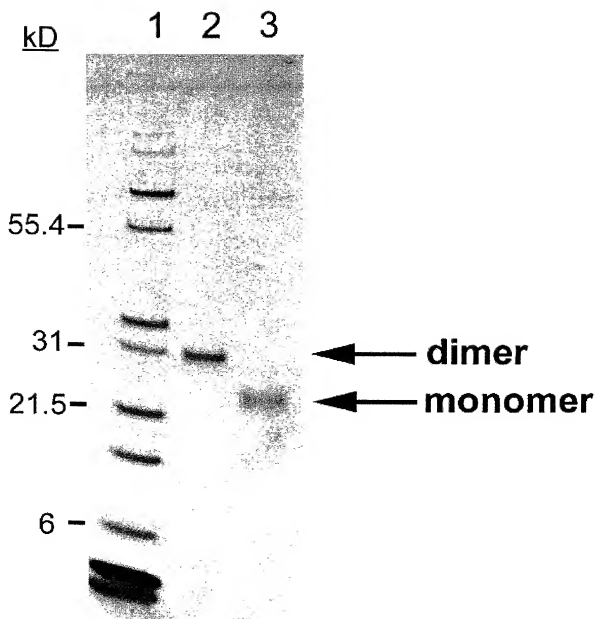
FIG. 29

FIG. 30A   FIG. 30B
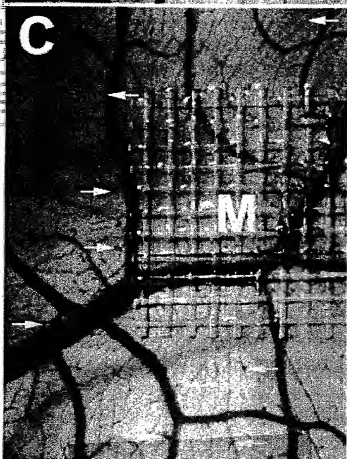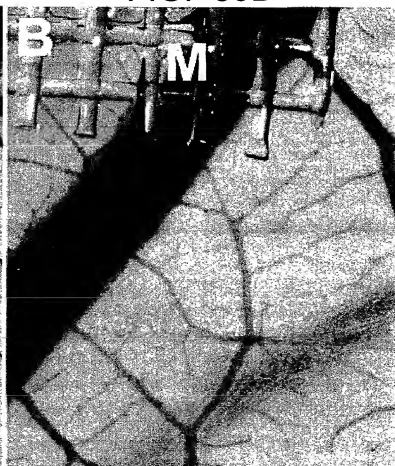
FIG. 30C   FIG. 30D

FIG. 31A PBS

FIG. 31B PDGF-CC

FIG. 31C FGF-2

FIG. 31D VEGF
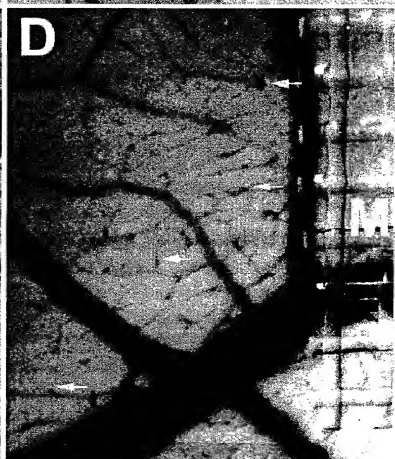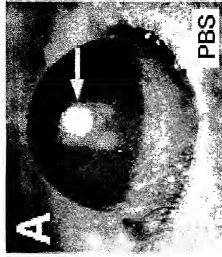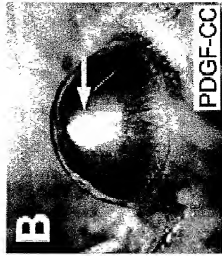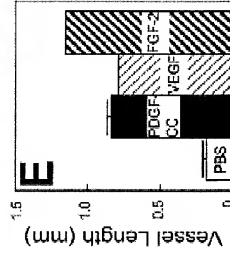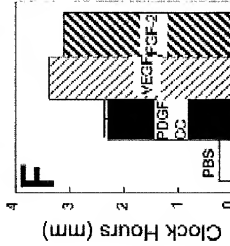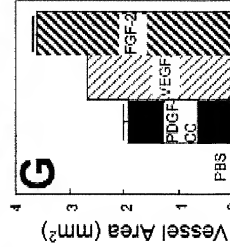
FIG. 31E

FIG. 31F

FIG. 31G
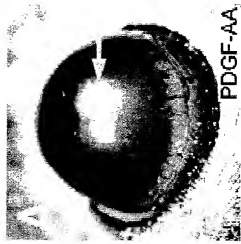
FIG. 32A   FIG. 32B   FIG. 32C   FIG. 32D

PDGF-AA   PDGF-AB   PDGF-BB   PDGF-CC

FIG. 32E   FIG. 32F   FIG. 32G

FIG. 33A   FIG. 33B

A   PDGF-AA

B   PDGF-AB

C   PDGF-BB

D   PDGF-CC

FIG. 33C   FIG. 33D

E   Vessel Count

FIG. 33E